IN THE SPECIFICATION

Please amend the abstract of the application as shown below:

The invention provides a target and methods for specific binding and inhibition of RlmA proteins from bacterial species. The invention is directed to a method for identifying compounds that bind to a bacterial RlmA-binding pocket, comprising preparing a reaction solution comprising the compound to be tested and an entity comprising a bacterial RlmA-binding pocket and detecting the presence or amount of binding. The invention has applications in control of bacterial gene expression, control of bacterial growth, antibacterial chemistry, and antibacterial therapy.

Please amend paragraph 0027 of the application as published, as follows:

FIG. 2A illustrates a ribbon representation of an asymmetric dimer, as found in the crystal structure, showing a well-defined RNA-binding cleft. The deep W-shaped cleft has two Zn-fingers at the top and two SAM molecules at the bottom. FIG. 2B illustrates a stereo view of the novel Zn-finger motif of $RlmA^I$ FIG. 2B illustrates a stereo view of SAM binding region of an $RmlA^I$ molecule. The |Fo|-|Fc|electron density mesh covering the SAM molecule was calculated at 2.8 Å resolution based on the phasing by protein atoms only. FIG. 2C demonstrates that difference electron density maps clearly define the mode of binding of SAM in the $RlmA^I$ enzyme structure.

Please amend the section entitled "CROSS-REFERENCE TO RELATED APPLICATIONS" as follows:

CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a National Stage application of International Application PCT/US04/20244, filed on June 26, 2004 which claims priority to provisional application[[:]] 06/482,722 filed Jun. 27, 2003, the contents of which are incorporated herein by reference.

Please amend paragraph 0072 of the application as published as follows:

Libraries of RNA oligonucleotides for use in screening can also be generated by combinatorial chemical synthesis. RNA molecules that bind to RlmA can be isolated form these libraries using affinity purification by RlmA, and then amplified and sequence by RT-PCR methods, in which the RNA sequence is first converted to DNA using reverse transciptase, the resulting DNA is then amplified by polymerase chain reaction (PCR) methods, and the amplified DNA is then cloned and sequenced by conventional DNA sequencing methods. The corresponding RNA molecules can then be chemically synthesized in sufficient quantities for assay, and evaluated for their ability to inhibit RlmA-rRNA interactions. Related SELEX methods can also be used in a similar way to identify RNA oligonucleotides that bind to RlmA and are potential inhibitors of RlmA-rRNA interactions. (Famulok, M.; Szostak, J. W., In Vitro Selection of Specific Ligand Binding Nucleic Acids. Angew. Chem. 1992, 104, 1001. (Angew. Chem. Int. Ed. Engl. 1992, 31, 979-988.); Famulok, M.; Szostak, J. W., Selection of Functional RNA and DNA Molecules from Randomized Sequences. Nucleic Acids and Molecular Biology, Vol 7, F. Eckstein, D. M. J. Lilley, Eds., Springer Verlag, Berlin, 1993, pp. 271; Klug, S.; Famulok, M., All you wanted to know about SELEX. Mol. Biol. Reports 1994, 20, 97-107; Burgstaller, P.; Famulok, M. Synthetic ribozymes and the first deoxyribozyme. Angew. Chem. 1995, 107, 1303-1306 (Angew. Chem. Int. Ed. Engl. 1995, 34, 1189-1192). ~~See also http://www.lmb.uni-muenchen.de/groups/famulok/SELEX.html for a description of the SELEX method.~~